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      Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg Cys Arg Pro Phe Asn
          15                  20                  25
      ttg gca gag cgg aaa gct agc gcc cat tca ata gta gaa tgt gat cct       145
      Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro
      30                  35                  40                  45
      gta cga aaa gaa gtt agt gta cga act gga gga ttg gct gac aag agc       193
      Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser
                      50                  55                  60
      tca agg aaa aca tac act ttt gat atg gtg ttt gga gca tct act aaa       241
      Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys
                  65                  70                  75
      cag att gat gtt tac cga agt gtt gtt tgt cca att ctg gat gaa gtt       289
      Gln Ile Asp Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val
              80                  85                  90
      att atg ggc tat aat tgc act atc ttt gcg tat ggc caa act ggc act       337
      Ile Met Gly Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr
          95                  100                 105
      gga aaa act ttt aca atg gaa ggt gaa agg tca cct aat gaa gag tat       385
      Gly Lys Thr Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu Glu Tyr
      110                 115                 120                 125
      acc tgg gaa gag gat ccc ttg gct ggt ata att cca cgt acc ctt cat       433
      Thr Trp Glu Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His
                      130                 135                 140
      caa att ttt gag aaa ctt act gat aat ggt act gaa ttt tca gtc aaa       481
      Gln Ile Phe Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser Val Lys
                  145                 150                 155
      gtg tct ctg ttg gag atc tat aat gaa gag ctt ttt gat ctt ctt aat       529
      Val Ser Leu Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu Leu Asn
              160                 165                 170
      cca tca tct gat gtt tct gag aga cta cag atg ttt gat gat ccc cgt       577
      Pro Ser Ser Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg
          175                 180                 185
      aac aag aga gga gtg ata att aaa ggt tta gaa gaa att aca gta cac       625
      Asn Lys Arg Gly Val Ile Ile Lys Gly Leu Glu Glu Ile Thr Val His
      190                 195                 200                 205
      aac aag gat gaa gtc tat caa att tta gaa aag ggg gca gca aaa agg       673
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                      210                 215                 220
      aca act gca gct act ctg atg aat gca tac tct agt cgt tcc cac tca       721
      Thr Thr Ala Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser His Ser
                  225                 230                 235
      gtt ttc tct gtt aca ata cat atg aaa gaa act acg att gat gga gaa       769
      Val Phe Ser Val Thr Ile His Met Lys Glu Thr Thr Ile Asp Gly Glu
              240                 245                 250
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          255                 260                 265
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Gly Asn Ile Asn Gln Ser Leu Leu Thr Leu Gly Arg Val Ile Thr Ala
                290                 295                 300
ctt gta gaa aga aca cct cat gtt cct tat cga gaa tct aaa cta act      961
Leu Val Glu Arg Thr Pro His Val Pro Tyr Arg Glu Ser Lys Leu Thr
            305                 310                 315
aga atc ctc cag gat tct ctt gga ggg cgt aca aga aca tct ata att     1009
Arg Ile Leu Gln Asp Ser Leu Gly Gly Arg Thr Arg Thr Ser Ile Ile
        320                 325                 330
gca aca att tct cct gca tct ctc aat ctt gag gaa act ctg agt aca     1057
Ala Thr Ile Ser Pro Ala Ser Leu Asn Leu Glu Glu Thr Leu Ser Thr
    335                 340                 345
ttg gaa tat gct cat aga gca aag aac ata ttg aat aag cct gaa gtg     1105
Leu Glu Tyr Ala His Arg Ala Lys Asn Ile Leu Asn Lys Pro Glu Val
350                 355                 360                 365
aat cag aaa ctc acc aaa aaa gct ctt att aag gag tat acg gag gag     1153
Asn Gln Lys Leu Thr Lys Lys Ala Leu Ile Lys Glu Tyr Thr Glu Glu
                370                 375                 380
ata gaa cgt tta aaa cga gat ctt gct gca gcc cgt gag aaa aat gga     1201
Ile Glu Arg Leu Lys Arg Asp Leu Ala Ala Ala Arg Glu Lys Asn Gly
            385                 390                 395
gtg tat att tct gaa gaa aat ttt aga gtc atg agt gga aaa tta act     1249
Val Tyr Ile Ser Glu Glu Asn Phe Arg Val Met Ser Gly Lys Leu Thr
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gtt caa gaa gag cag att gta gaa ttg att gaa aaa att ggt gct gtt     1297
Val Gln Glu Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly Ala Val
    415                 420                 425
gag gag gag ctg aat agg gtt aca gag ttg ttt atg gat aat aaa aat     1345
Glu Glu Glu Leu Asn Arg Val Thr Glu Leu Phe Met Asp Asn Lys Asn
430                 435                 440                 445
gaa ctt gac cag tgt aaa tct gac ctg caa aat aaa aca caa gaa ctt     1393
Glu Leu Asp Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln Glu Leu
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gaa acc act caa aaa cat ttg caa gaa act aaa tta caa ctt gtt aaa     1441
Glu Thr Thr Gln Lys His Leu Gln Glu Thr Lys Leu Gln Leu Val Lys
            465                 470                 475
gaa gaa tat atc aca tca gct ttg gaa agt act gag gag aaa ctt cat     1489
Glu Glu Tyr Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys Leu His
        480                 485                 490
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Asp Ala Ala Ser Lys Leu Leu Asn Thr Val Glu Glu Thr Thr Lys Asp
    495                 500                 505
gta tct ggt ctc cat tcc aaa ctg gat cgt aag aag gca gtt gac caa     1585
Val Ser Gly Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val Asp Gln
510                 515                 520                 525
cac aat gca gaa gct cag gat att ttt ggc aaa aac ctg aat agt ctg     1633
His Asn Ala Glu Ala Gln Asp Ile Phe Gly Lys Asn Leu Asn Ser Leu
                530                 535                 540
ttt aat aat atg gaa gaa tta att aag gat ggc agc tca aag caa aag     1681
Phe Asn Asn Met Glu Glu Leu Ile Lys Asp Gly Ser Ser Lys Gln Lys
            545                 550                 555
gcc atg cta gaa gta cat aag acc tta ttt ggt aat ctg ctg tct tcc     1729
Ala Met Leu Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu Ser Ser
        560                 565                 570
agt gtc tct gca tta gat acc att act aca gta gca ctt gga tct ctc     1777
Ser Val Ser Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly Ser Leu
    575                 580                 585
aca tct att cca gaa aat gtg tct act cat gtt tct cag att ttt aat     1825
Thr Ser Ile Pro Glu Asn Val Ser Thr His Val Ser Gln Ile Phe Asn
590                 595                 600                 605
atg ata cta aaa gaa caa tca tta gca gca gaa agt aaa act gta cta     1873
Met Ile Leu Lys Glu Gln Ser Leu Ala Ala Glu Ser Lys Thr Val Leu
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cta aag cat att ttc aag act tca ttg aca gtg gcc gat aag ata gaa     2017
Leu Lys His Ile Phe Lys Thr Ser Leu Thr Val Ala Asp Lys Ile Glu
    655                 660                 665
gat caa aaa aaa agg aac tca gat ggc ttt ctc agt ata ctg tgt aac     2065
Asp Gln Lys Lys Arg Asn Ser Asp Gly Phe Leu Ser Ile Leu Cys Asn
670                 675                 680                 685
aat cta cat gaa cta caa gaa aat acc att tgt tcc ttg gtt gag tca     2113
Asn Leu His Glu Leu Gln Glu Asn Thr Ile Cys Ser Leu Val Glu Ser
                690                 695                 700
caa aag caa tgt gga aac cta act gaa gac ctg aag aca ata aag cag     2161
Gln Lys Gln Cys Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys Gln
            705                 710                 715
acc cat tcc cag gaa ctt tgc aag tta atg aat ctt tgg aca gag aga     2209
Thr His Ser Gln Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu Arg
        720                 725                 730
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Phe Cys Ala Leu Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu Ser
    735                 740                 745
agt gtc cag gaa aat ata cag cag aaa tct aag gat ata gtc aac aaa     2305
Ser Val Gln Glu Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn Lys
750                 755                 760                 765
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                770                 775                 780
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            785                 790                 795
tct gtg aaa cac tct gat aaa ctc aat ggc aac ctg gaa aaa ata tct     2449
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        800                 805                 810
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Phe Ser Glu Gln Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu Leu
830                 835                 840                 845
cac aac tta ttg gag gtt gta agc caa tgt tgt gag gct tca agt tca     2593
His Asn Leu Leu Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser Ser
                850                 855                 860
gac atc act gag aaa tca gat gga cgt aag gca gct cat gag aaa cag     2641
Asp Ile Thr Glu Lys Ser Asp Gly Arg Lys Ala Ala His Glu Lys Gln
            865                 870                 875
cat aac att ttt ctt gat cag atg act att gat gaa gat aaa ttg ata     2689
His Asn Ile Phe Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu Ile
        880                 885                 890
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910                 915                 920                 925
acg aca cca cag agg aaa agt tat tta tac cca tca aca ctg gta aga     2833
Thr Thr Pro Gln Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val Arg
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act gaa cca cgt gaa cat ctc ctt gat cag ctg aaa agg aaa cag cct     2881
Thr Glu Pro Arg Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln Pro
            945                 950                 955
gag ctg tta atg atg cta aac tgt tca gaa aac aac aaa gaa gag aca     2929
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990                 995                 1000                1005
tca att ggc ggg gtt  cca ttt ttc cag cat  aaa aaa tca cat gga       3070
Ser Ile Gly Gly Val  Pro Phe Phe Gln His  Lys Lys Ser His Gly
                1010                1015                1020
aaa gac aaa gaa aac  aga ggc att aac aca  ctg gag agg tct aaa       3115
Lys Asp Lys Glu Asn  Arg Gly Ile Asn Thr  Leu Glu Arg Ser Lys
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Val Glu Glu Thr Thr  Glu His Leu Val Thr  Lys Ser Arg Leu Pro
                1040                1045                1050
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ttctgtcatc cctatagttc actttgtatt aaattgggtt tcatttggga tttgcaatgt   3694
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; Sequence 135431, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135431
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-135431

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Qy          3 GTGGAATTATACCAGCCA 20
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Db          5 GAGGCATTATACCAGCCA 22
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SCORE 1.3 BuildDate: 12/06/2005

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; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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Previous Sequence

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Here is the list of the requested sequences:

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